



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Anderson, Darrell R.
- (ii) TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 - (B) STREET: 699 Prince Street
 - (C) CITY: Alexandria
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22314
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/487,550
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Teskin, Robin L.
 - (B) REGISTRATION NUMBER: 35,030
 - (C) REFERENCE/DOCKET NUMBER: 012712-131
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 703 836 6620
 - (B) TELEFAX: 703 836 2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

60

(A) NAME/KEY: CDS
 (B) LOCATION: 1..705

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	48
Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10					15			
GGT	GCA	CGA	TGT	GCC	TAT	GAA	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	96
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	
			20					25					30			
TCC	CCA	GGA	CAG	ACG	GCC	AGG	ATC	ACC	TGT	GGG	GGA	GAC	AAC	AGT	AGA	144
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg	
		35					40					45				
AAT	GAA	TAT	GTC	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GCG	CGG	GCC	CCT	ATA	192
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile	
	50					55				60						
CTG	GTC	ATC	TAT	GAT	GAT	AGT	GAC	CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA	240
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
65					70					75					80	
TTC	TCT	GGC	TCC	AAA	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AAC	GGG	288
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly	
				85					90					95		
GTC	GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGG	336
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	
			100					105					110			
GCT	AGT	GAT	CAT	CCG	GTC	TTC	GGA	GGA	GGG	ACC	CGG	GTG	ACC	GTC	CTA	384
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu	
		115					120					125				
GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	432
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	
	130					135					140					
GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	480
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	
145					150					155					160	
TTC	TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	528
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	
			165						170					175		
GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	576
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	

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180										185					190					
AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG	624				
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys					
		195					200					205								
TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG	672				
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val					
		210				215					220									
GAG	AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA						705				
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*										
225					230					235										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10					15			
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	
			20					25					30			
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg	
		35					40					45				
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile	
	50					55					60					
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
65				70				75						80		
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly	
				85				90						95		
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	
			100					105					110			
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu	
		115					120					125				
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	
	130					135					140					
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	
145					150					155					160	

Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	
				165					170					175		
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	
			180					185					190			
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	
		195					200					205				
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	
	210					215					220					
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*						
225					230					235						

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1431

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCT	CCC	AGA	TGG	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		
GTC	CTG	TCC	CAG	GTG	AAG	CTG	CAG	CAG	TGG	GGC	GAA	GGA	CTT	CTG	CAG	96
Val	Leu	Ser	Gln	Val	Lys	Leu	Gln	Gln	Trp	Gly	Glu	Gly	Leu	Leu	Gln	
			20					25					30			
CCT	TCG	GAG	ACC	CTG	TCC	CGC	ACC	TGC	GTT	GTC	TCT	GGT	GGC	TCC	ATC	144
Pro	Ser	Glu	Thr	Leu	Ser	Arg	Thr	Cys	Val	Val	Ser	Gly	Gly	Ser	Ile	
		35				40						45				
AGC	GGT	TAC	TAC	TAC	TGG	ACC	TGG	ATC	CGC	CAG	ACC	CCA	GGG	AGG	GGA	192
Ser	Gly	Tyr	Tyr	Tyr	Trp	Thr	Trp	Ile	Arg	Gln	Thr	Pro	Gly	Arg	Gly	
	50					55				60						
CTG	GAG	TGG	ATT	GGC	CAT	ATT	TAT	GGT	AAT	GGT	GCG	ACC	ACC	AAC	TAC	240
Leu	Glu	Trp	Ile	Gly	His	Ile	Tyr	Gly	Asn	Gly	Ala	Thr	Thr	Asn	Tyr	
65					70				75						80	

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AAT Asn	CCC Pro	TCC Ser	CTC Leu	AAG Lys 85	AGT Ser	CGA Arg	GTC Val	ACC Thr	ATT Ile 90	TCA Ser	AAA Lys	GAC Asp	ACG Thr	TCC Ser 95	AAG Lys	288
AAC Asn	CAG Gln	TTC Phe	TTC Phe 100	CTG Leu	AAC Asn	TTG Leu	AAT Asn	TCT Ser 105	GTG Val	ACC Thr	GAC Asp	GCG Ala	GAC Asp 110	ACG Thr	GCC Ala	336
GTC Val	TAT Tyr	TAC Tyr 115	TGT Cys	GCG Ala	AGA Arg	GGC Gly	CCT Pro 120	CGC Arg	CCT Pro	GAT Asp	TGC Cys 125	ACA Thr	ACC Thr	ATT Ile	TGT Cys	384
TAT Tyr 130	GGC Gly	GGC Gly	TGG Trp	GTC Val	GAT Asp	GTC Val 135	TGG Trp	GGC Gly	CCG Pro	GGA Gly	GAC Asp 140	CTG Leu	GTC Val	ACC Thr	GTC Val	432
TCC Ser 145	TCA Ser	GCT Ala	AGC Ser	ACC Thr	AAG Lys 150	GGC Gly	CCA Pro	TCG Ser	GTC Val	TTC Phe 155	CCC Pro	CTG Leu	GCA Ala	CCC Pro	TCC Ser 160	480
TCC Ser	AAG Lys	AGC Ser	ACC Thr	TCT Ser 165	GGG Gly	GGC Gly	ACA Thr	GCG Ala	GCC Ala 170	CTG Leu	GGC Gly	TGC Cys	CTG Leu	GTC Val 175	AAG Lys	528
GAC Asp	TAC Tyr	TTC Phe	CCC Pro 180	GAA Glu	CCG Pro	GTG Val	ACG Thr	GTG Val 185	TCG Ser	TGG Trp	AAC Asn	TCA Ser	GGC Gly 190	GCC Ala	CTG Leu	576
ACC Thr	AGC Ser	GGC Gly 195	GTG Val	CAC His	ACC Thr	TTC Phe 200	CCG Pro	GCT Ala	GTC Val	CTA Leu	CAG Gln	TCC Ser 205	TCA Ser	GGA Gly	CTC Leu	624
TAC Tyr 210	TCC Ser	CTC Leu	AGC Ser	AGC Ser	GTG Val	GTG Val 215	ACC Thr	GTG Val	CCC Pro	TCC Ser	AGC Ser 220	AGC Ser	TTG Leu	GGC Gly	ACC Thr	672
CAG Gln 225	ACC Thr	TAC Tyr	ATC Ile	TGC Cys	AAC Asn 230	GTG Val	AAT Asn	CAC His	AAG Lys	CCC Pro 235	AGC Ser	AAC Asn	ACC Thr	AAG Lys	GTG Val 240	720
GAC Asp	AAG Lys	AAA Lys	GCA Ala	GAG Glu 245	CCC Pro	AAA Lys	TCT Ser	TGT Cys	GAC Asp 250	AAA Lys	ACT Thr	CAC His	ACA Thr	TGC Cys 255	CCA Pro	768
CCG Pro	TGC Cys	CCA Pro	GCA Ala 260	CCT Pro	GAA Glu	CTC Leu	CTG Leu	GGG Gly 265	GGA Gly	CCG Pro	TCA Ser	GTC Val	TTC Phe 270	CTC Leu	TTC Phe	816
CCC Pro	CCA Pro	AAA Lys 275	CCC Pro	AAG Lys	GAC Asp	ACC Thr	CTC Leu 280	ATG Met	ATC Ile	TCC Ser	CGG Arg	ACC Thr 285	CCT Pro	GAG Glu	GTC Val	864
ACA Thr 290	TGC Cys	GTG Val	GTG Val	GTG Val	GAC Asp	GTG Val 295	AGC Ser	CAC His	GAA Glu	GAC Asp	CCT Pro 300	GAG Glu	GTC Val	AAG Lys	TTC Phe	912

AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	960
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
305					310					315					320	
CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	1008
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
				325					330					335		
GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	1056
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
			340					345					350			
TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	1104
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
		355					360					365				
AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	1152
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
	370					375					380					
GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	1200
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
385					390					395					400	
TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	1248
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
				405					410					415		
GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	1296
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
			420					425					430			
TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	1344
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
		435					440					445				
GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	1392
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	
	450					455					460					
TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA				1431
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	*				
465					470					475						

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

65

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1				5					10					15	
Val	Leu	Ser	Gln	Val	Lys	Leu	Gln	Gln	Trp	Gly	Glu	Gly	Leu	Leu	Gln
			20				25						30		
Pro	Ser	Glu	Thr	Leu	Ser	Arg	Thr	Cys	Val	Val	Ser	Gly	Gly	Ser	Ile
		35					40					45			
Ser	Gly	Tyr	Tyr	Tyr	Trp	Thr	Trp	Ile	Arg	Gln	Thr	Pro	Gly	Arg	Gly
	50					55					60				
Leu	Glu	Trp	Ile	Gly	His	Ile	Tyr	Gly	Asn	Gly	Ala	Thr	Thr	Asn	Tyr
65					70					75					80
Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys
				85					90					95	
Asn	Gln	Phe	Phe	Leu	Asn	Leu	Asn	Ser	Val	Thr	Asp	Ala	Asp	Thr	Ala
			100					105					110		
Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Arg	Pro	Asp	Cys	Thr	Thr	Ile	Cys
		115					120					125			
Tyr	Gly	Gly	Trp	Val	Asp	Val	Trp	Gly	Pro	Gly	Asp	Leu	Val	Thr	Val
	130					135					140				
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser
145					150					155					160
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
				165					170					175	
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
			180					185					190		
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
		195					200					205			
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
	210					215					220				
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
225					230					235					240
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
				245					250					255	
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
			260					265					270		
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
		275					280					285			
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
	290					295					300				

Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
305					310					315					320
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
				325					330					335	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
			340					345					350		
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
		355					360					365			
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
	370					375					380				
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
385					390					395					400
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
				405					410					415	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
			420					425					430		
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
		435					440					445			
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
	450					455					460				
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	*			
465					470					475					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC CTC CCT GCT CAG CTC CTC GGG CTG CTA TTG CTC TGC GTC CCC

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Met 1	Ser	Leu	Pro	Ala 5	Gln	Leu	Leu	Gly	Leu 10	Leu	Leu	Leu	Cys	Val 15	Pro	
GGG Gly	TCC Ser	AGT Ser	GGG Gly 20	GAA Glu	GTT Val	GTG Val	ATG Met	ACT Thr 25	CAG Gln	TCT Ser	CCA Pro	CTG Leu	TCC Ser 30	CTT Leu	CCC Pro	96
ATC Ile	ACA Thr	CCT Pro 35	GGA Gly	GAG Glu	CCG Pro	GCC Ala	TCC Ser 40	ATC Ile	TCC Ser	TGT Cys	AGG Arg	TCT Ser 45	AGT Ser	CAA Gln	AGC Ser	144
CTT Leu	AAA Lys 50	CAC His	AGT Ser	AAT Asn	GGA Gly	GAC Asp 55	ACC Thr	TTC Phe	CTG Leu	AGT Ser	TGG Trp 60	TAT Tyr	CAG Gln	CAG Gln	AAG Lys	192
CCA Pro 65	GGC Gly	CAA Gln	CCT Pro	CCA Pro	AGG Arg 70	CTC Leu	CTG Leu	ATT Ile	TAT Tyr	AAG Lys 75	GTT Val	TCT Ser	AAC Asn	CGG Arg	GAC Asp 80	240
TCT Ser	GGG Gly	GTC Val	CCA Pro	GAC Asp 85	AGA Arg	TTC Phe	AGC Ser	GGC Gly	AGT Ser 90	GGG Gly	GCA Ala	GGG Gly	ACA Thr	GAT Asp 95	TTC Phe	288
ACA Thr	CTG Leu	AAA Lys	ATC Ile 100	AGC Ser	GCA Ala	GTG Val	GAG Glu	GCT Ala 105	GAA Glu	GAT Asp	GTT Val	GGG Gly	GTT Val 110	TAT Tyr	TTC Phe	336
TGC Cys	GGG Gly	CAA Gln 115	GGT Gly	ACA Thr	AGG Arg	ACT Thr	CCT Pro 120	CCC Pro	ACT Thr	TTC Phe	GGC Gly	GGA Gly 125	GGG Gly	ACC Thr	AAG Lys	384
GTG Val 130	GAA Glu	ATC Ile	AAA Lys	CGT Arg	ACG Thr	GTG Val 135	GCT Ala	GCA Ala	CCA Pro	TCT Ser	GTC Val 140	TTC Phe	ATC Ile	TTC Phe	CCG Pro	432
CCA Pro 145	TCT Ser	GAT Asp	GAG Glu	CAG Gln	TTG Leu	AAA Lys 150	TCT Ser	GGA Gly	ACT Thr	GCC Ala 155	TCT Ser	GTT Val	GTG Val	TGC Cys	CTG Leu 160	480
CTG Leu	AAT Asn	AAC Asn	TTC Phe 165	TAT Tyr	CCC Pro	AGA Arg	GAG Glu	GCC Ala 170	AAA Lys	GTA Val	CAG Gln	TGG Trp	AAG Lys 175	GTG Val	GAT Asp	528
AAC Asn	GCC Ala	CTC Leu	CAA Gln 180	TCG Ser	GGT Gly	AAC Asn	TCC Ser	CAG Gln 185	GAG Glu	AGT Ser	GTC Val	ACA Thr	GAG Glu 190	CAG Gln	GAC Asp	576
AGC Ser	AAG Lys	GAC Asp 195	AGC Ser	ACC Thr	TAC Tyr	AGC Ser	CTC Leu 200	AGC Ser	AGC Ser	ACC Thr	CTG Leu	ACG Thr 205	CTG Leu	AGC Ser	AAA Lys	624
GCA Ala 210	GAC Asp	TAC Tyr	GAG Glu	AAA Lys	CAC His	AAA Lys 215	GTC Val	TAC Tyr	GCC Ala	TGC Cys	GAA Glu 220	GTC Val	ACC Thr	CAT His	CAG Gln	672
GGC	CTG	AGC	TCG	CCC	GTC	ACA	AAG	AGC	TTC	AAC	AGG	GGA	GAG	TGT	TGA	720

Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	*
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Leu	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Cys	Val	Pro
1				5					10					15	
Gly	Ser	Ser	Gly	Glu	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro
			20					25					30		
Ile	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser
		35					40					45			
Leu	Lys	His	Ser	Asn	Gly	Asp	Thr	Phe	Leu	Ser	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Asp
65					70					75					80
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Lys	Ile	Ser	Ala	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Phe
			100					105					110		
Cys	Gly	Gln	Gly	Thr	Arg	Thr	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	130					135					140				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
145					150					155					160
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
				165					170					175	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			180					185					190		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		195					200					205			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	210					215					220				

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1437

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	48
Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	
1				5				10						15		
GTC	CAG	TGT	GAG	GTG	CAA	CTG	GTG	GAG	TCT	GGG	GGA	GGC	TTG	GTC	CAG	96
Val	Gln	Cys	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	
			20					25					30			
CCT	GGC	GGG	TCC	CTG	AGA	GTC	TCC	TGT	GCA	GTC	TCT	GGA	TTC	ACC	TTC	144
Pro	Gly	Gly	Ser	Leu	Arg	Val	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Phe	
			35				40					45				
AGT	GAC	CAC	TAC	ATG	TAT	TGG	TTC	CGC	CAG	GCT	CCA	GGG	AAG	GGG	CCG	192
Ser	Asp	His	Tyr	Met	Tyr	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Pro	
	50					55				60						
GAA	TGG	GTA	GGT	TTC	ATT	AGA	AAC	AAA	CCG	AAC	GGT	GGG	ACA	ACA	GAA	240
Glu	Trp	Val	Gly	Phe	Ile	Arg	Asn	Lys	Pro	Asn	Gly	Gly	Thr	Thr	Glu	
65				70				75							80	
TAC	GCC	GCG	TCT	GTG	AAA	GAC	AGA	TTC	ACC	ATC	TCC	AGA	GAT	GAT	TCC	288
Tyr	Ala	Ala	Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	
			85					90						95		
AAA	AGC	ATC	GCC	TAT	CTG	CAA	ATG	AGC	AGC	CTG	AAA	ATC	GAG	GAC	ACG	336
Lys	Ser	Ile	Ala	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ile	Glu	Asp	Thr	
			100					105					110			
GCC	GTC	TAT	TAC	TGT	ACT	ACA	TCC	TAC	ATT	TCA	CAT	TGT	CGG	GGT	GGT	384
Ala	Val	Tyr	Tyr	Cys	Thr	Thr	Ser	Tyr	Ile	Ser	His	Cys	Arg	Gly	Gly	

70

115					120					125							
GTC Val	TGC Cys 130	TAT Tyr	GGA Gly	GGT Gly	TAC Tyr	TTC Phe 135	GAA Glu	TTC Phe	TGG Trp	GGC Gly	CAG Gln 140	GGC Gly	GCC Ala	CTG Leu	GTC Val	432	
ACC Thr 145	GTC Val	TCC Ser	TCA Ser	GCT Ala	AGC Ser 150	ACC Thr	AAG Lys	GGC Gly	CCA Pro	TCG Ser 155	GTC Val	TTC Phe	CCC Pro	CTG Leu	GCA Ala 160	480	
CCC Pro	TCC Ser	TCC Ser	AAG Lys	AGC Ser 165	ACC Thr	TCT Ser	GGG Gly	GGC Gly	ACA Thr 170	GCG Ala	GCC Ala	CTG Leu	GGC Gly	TGC Cys 175	CTG Leu	528	
GTC Val	AAG Lys	GAC Asp	TAC Tyr 180	TTC Phe	CCC Pro	GAA Glu	CCG Pro	GTG Val 185	ACG Thr	GTG Val	TCG Ser	TGG Trp	AAC Asn 190	TCA Ser	GGC Gly	576	
GCC Ala	CTG Leu	ACC Thr 195	AGC Ser	GGC Gly	GTG Val	CAC His	ACC Thr 200	TTC Phe	CCG Pro	GCT Ala	GTC Val	CTA Leu 205	CAG Gln	TCC Ser	TCA Ser	624	
GGA Gly	CTC Leu 210	TAC Tyr	TCC Ser	CTC Leu	AGC Ser	AGC Ser 215	GTG Val	GTG Val	ACC Thr	GTG Val	CCC Pro 220	TCC Ser	AGC Ser	AGC Ser	TTG Leu	672	
GGC Gly 225	ACC Thr	CAG Gln	ACC Thr	TAC Tyr	ATC Ile 230	TGC Cys	AAC Asn	GTG Val	AAT Asn	CAC His 235	AAG Lys	CCC Pro	AGC Ser	AAC Asn	ACC Thr 240	720	
AAG Lys	GTG Val	GAC Asp	AAG Lys	AAA Lys 245	GCA Ala	GAG Glu	CCC Pro	AAA Lys	TCT Ser 250	TGT Cys	GAC Asp	AAA Lys	ACT Thr	CAC His 255	ACA Thr	768	
TGC Cys	CCA Pro	CCG Pro	TGC Cys 260	CCA Pro	GCA Ala	CCT Pro	GAA Glu	CTC Leu 265	CTG Leu	GGG Gly	GGA Gly	CCG Pro	TCA Ser 270	GTC Val	TTC Phe	816	
CTC Leu	TTC Phe	CCC Pro 275	CCA Pro	AAA Lys	CCC Pro	AAG Lys	GAC Asp 280	ACC Thr	CTC Leu	ATG Met	ATC Ile	TCC Ser 285	CGG Arg	ACC Thr	CCT Pro	864	
GAG Glu	GTC Val 290	ACA Thr	TGC Cys	GTG Val	GTG Val	GTG Val 295	GAC Asp	GTG Val	AGC Ser	CAC His	GAA Glu 300	GAC Asp	CCT Pro	GAG Glu	GTC Val	912	
AAG Lys 305	TTC Phe	AAC Asn	TGG Trp	TAC Tyr	GTG Val 310	GAC Asp	GGC Gly	GTG Val	GAG Glu	GTG Val 315	CAT His	AAT Asn	GCC Ala	AAG Lys	ACA Thr 320	960	
AAG Lys	CCG Pro	CGG Arg	GAG Glu	GAG Glu 325	CAG Gln	TAC Tyr	AAC Asn	AGC Ser	ACG Thr 330	TAC Tyr	CGT Arg	GTG Val	GTC Val	AGC Ser 335	GTC Val	1008	
CTC Leu	ACC Thr	GTC Val	CTG Leu	CAC His	CAG Gln	GAC Asp	TGG Trp	CTG Leu	AAT Asn	GGC Gly	AAG Lys	GAG Glu	TAC Tyr	AAG Lys	TGC Cys	1056	

340						345						350					
AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	1104	
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser		
		355					360					365					
AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	1152	
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro		
	370					375					380						
TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	1200	
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val		
	385				390					395					400		
AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	1248	
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly		
				405					410					415			
CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	1296	
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp		
			420					425					430				
GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	1344	
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp		
		435					440					445					
CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	1392	
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His		
	450					455					460						
AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA		1437	
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	*			
	465				470					475							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45

Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro

50					55					60					
Glu 65	Trp	Val	Gly	Phe	Ile 70	Arg	Asn	Lys	Pro	Asn 75	Gly	Gly	Thr	Thr	Glu 80
Tyr	Ala	Ala	Ser	Val 85	Lys	Asp	Arg	Phe	Thr 90	Ile	Ser	Arg	Asp	Asp 95	Ser
Lys	Ser	Ile	Ala 100	Tyr	Leu	Gln	Met	Ser 105	Ser	Leu	Lys	Ile	Glu 110	Asp	Thr
Ala	Val	Tyr 115	Tyr	Cys	Thr	Thr	Ser 120	Tyr	Ile	Ser	His	Cys 125	Arg	Gly	Gly
Val 130	Cys	Tyr	Gly	Gly	Tyr	Phe 135	Glu	Phe	Trp	Gly	Gln 140	Gly	Ala	Leu	Val
Thr 145	Val	Ser	Ser	Ala	Ser 150	Thr	Lys	Gly	Pro	Ser 155	Val	Phe	Pro	Leu	Ala 160
Pro	Ser	Ser	Lys	Ser 165	Thr	Ser	Gly	Gly	Thr 170	Ala	Ala	Leu	Gly	Cys 175	Leu
Val	Lys	Asp	Tyr 180	Phe	Pro	Glu	Pro	Val 185	Thr	Val	Ser	Trp	Asn 190	Ser	Gly
Ala	Leu	Thr 195	Ser	Gly	Val	His 200	Thr	Phe	Pro	Ala	Val	Leu 205	Gln	Ser	Ser
Gly 210	Leu	Tyr	Ser	Leu	Ser	Ser 215	Val	Val	Thr	Val	Pro 220	Ser	Ser	Ser	Leu
Gly 225	Thr	Gln	Thr	Tyr	Ile 230	Cys	Asn	Val	Asn	His 235	Lys	Pro	Ser	Asn	Thr 240
Lys	Val	Asp	Lys	Lys 245	Ala	Glu	Pro	Lys	Ser 250	Cys	Asp	Lys	Thr	His 255	Thr
Cys	Pro	Pro	Cys 260	Pro	Ala	Pro	Glu	Leu 265	Leu	Gly	Gly	Pro	Ser 270	Val	Phe
Leu	Phe 275	Pro	Pro	Lys	Pro	Lys	Asp 280	Thr	Leu	Met	Ile	Ser 285	Arg	Thr	Pro
Glu 290	Val	Thr	Cys	Val	Val 295	Val	Asp	Val	Ser	His	Glu 300	Asp	Pro	Glu	Val
Lys 305	Phe	Asn	Trp	Tyr	Val 310	Asp	Gly	Val	Glu	Val 315	His	Asn	Ala	Lys	Thr 320
Lys	Pro	Arg	Glu	Glu 325	Gln	Tyr	Asn	Ser	Thr 330	Tyr	Arg	Val	Val	Ser 335	Val
Leu	Thr	Val	Leu 340	His	Gln	Asp	Trp	Leu 345	Asn	Gly	Lys	Glu	Tyr 350	Lys	Cys

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 355 360 365
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 370 375 380
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 405 410 415
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 435 440 445
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 450 455 460
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
 465 470 475

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..711

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	48
Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10					15			
GGT	GCA	CGA	TGT	GAG	TCT	GTC	CTG	ACA	CAG	CCG	CCC	TCA	GTG	TCT	GGG	96
Gly	Ala	Arg	Cys	Glu	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	
			20					25					30			
GCC	CCA	GGG	CAG	AAG	GTC	ACC	ATC	TCG	TGC	ACT	GGG	AGC	ACC	TCC	AAC	144
Ala	Pro	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys	Thr	Gly	Ser	Thr	Ser	Asn	

35					40					45										
ATT	GGA	GGT	TAT	GAT	CTA	CAT	TGG	TAC	CAG	CAG	CTC	CCA	GGA	ACG	GCC	192				
Ile	Gly	Gly	Tyr	Asp	Leu	His	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala					
	50					55					60									
CCC	AAA	CTC	CTC	ATC	TAT	GAC	ATT	AAC	AAG	CGA	CCC	TCA	GGA	ATT	TCT	240				
Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ile	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Ser					
	65				70					75					80					
GAC	CGA	TTC	TCT	GGC	TCC	AAG	TCT	GGT	ACC	GCG	GCC	TCC	CTG	GCC	ATC	288				
Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ala	Ala	Ser	Leu	Ala	Ile					
				85				90						95						
ACT	GGG	CTC	CAG	ACT	GAG	GAT	GAG	GCT	GAT	TAT	TAC	TGC	CAG	TCC	TAT	336				
Thr	Gly	Leu	Gln	Thr	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr					
			100					105					110							
GAC	AGC	AGC	CTG	AAT	GCT	CAG	GTA	TTC	GGA	GGA	GGG	ACC	CGG	CTG	ACC	384				
Asp	Ser	Ser	Leu	Asn	Ala	Gln	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr					
		115					120					125								
GTC	CTA	GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	432				
Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro					
	130					135					140									
TCC	TCT	GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	480				
Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile					
	145				150					155					160					
AGT	GAC	TTC	TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	528				
Ser	Asp	Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser					
				165					170					175						
AGC	CCC	GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	576				
Ser	Pro	Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser					
			180					185					190							
AAC	AAC	AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	624				
Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln					
		195					200					205								
TGG	AAG	TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	672				
Trp	Lys	Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser					
	210					215					220									
ACC	GTG	GAG	AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA				711				
Thr	Val	Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*								
	225				230					235										

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

75

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met 1	Arg	Val	Pro	Ala 5	Gln	Leu	Leu	Gly	Leu 10	Leu	Leu	Leu	Trp	Leu 15	Pro
Gly	Ala	Arg	Cys 20	Glu	Ser	Val	Leu	Thr 25	Gln	Pro	Pro	Ser	Val 30	Ser	Gly
Ala	Pro	Gly 35	Gln	Lys	Val	Thr	Ile 40	Ser	Cys	Thr	Gly	Ser 45	Thr	Ser	Asn
Ile	Gly 50	Gly	Tyr	Asp	Leu	His 55	Trp	Tyr	Gln	Gln	Leu 60	Pro	Gly	Thr	Ala
Pro 65	Lys	Leu	Leu	Ile	Tyr 70	Asp	Ile	Asn	Lys	Arg 75	Pro	Ser	Gly	Ile	Ser 80
Asp	Arg	Phe	Ser	Gly 85	Ser	Lys	Ser	Gly	Thr 90	Ala	Ala	Ser	Leu	Ala 95	Ile
Thr	Gly	Leu	Gln 100	Thr	Glu	Asp	Glu	Ala 105	Asp	Tyr	Tyr	Cys	Gln 110	Ser	Tyr
Asp	Ser	Ser 115	Leu	Asn	Ala	Gln	Val 120	Phe	Gly	Gly	Gly	Thr 125	Arg	Leu	Thr
Val	Leu 130	Gly	Gln	Pro	Lys	Ala 135	Ala	Pro	Ser	Val	Thr 140	Leu	Phe	Pro	Pro
Ser 145	Ser	Glu	Glu	Leu	Gln 150	Ala	Asn	Lys	Ala	Thr 155	Leu	Val	Cys	Leu	Ile 160
Ser	Asp	Phe	Tyr	Pro 165	Gly	Ala	Val	Thr	Val 170	Ala	Trp	Lys	Ala	Asp 175	Ser
Ser	Pro	Val	Lys 180	Ala	Gly	Val	Glu	Thr 185	Thr	Thr	Pro	Ser	Lys 190	Gln	Ser
Asn	Asn	Lys 195	Tyr	Ala	Ala	Ser	Ser 200	Tyr	Leu	Ser	Leu	Thr 205	Pro	Glu	Gln
Trp	Lys 210	Ser	His	Arg	Ser	Tyr 215	Ser	Cys	Gln	Val	Thr 220	His	Glu	Gly	Ser
Thr 225	Val	Glu	Lys	Thr	Val 230	Ala	Pro	Thr	Glu	Cys 235	Ser	*			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1431 base pairs

(B) TYPE: nucleic acid

76

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1431

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCT	CCC	AGA	TGG	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		
GTC	CTG	TCC	CAG	GTG	CAG	CTG	CAG	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	
			20					25					30			
CCT	TCG	GAG	ACC	CTG	TCC	CTC	ACC	TGC	GCT	GTC	TCT	GGT	GGC	TCC	ATC	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile	
		35					40					45				
AGC	GGT	GGT	TAT	GGC	TGG	GGC	TGG	ATC	CGC	CAG	CCC	CCA	GGG	AAG	GGG	192
Ser	Gly	Gly	Tyr	Gly	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	
	50					55					60					
CTG	GAG	TGG	ATT	GGG	AGT	TTC	TAT	AGT	AGT	AGT	GGG	AAC	ACC	TAC	TAC	240
Leu	Glu	Trp	Ile	Gly	Ser	Phe	Tyr	Ser	Ser	Ser	Gly	Asn	Thr	Tyr	Tyr	
65					70				75					80		
AAC	CCC	TCC	CTC	AAG	AGT	CAA	GTC	ACC	ATT	TCA	ACA	GAC	ACG	TCC	AAG	288
Asn	Pro	Ser	Leu	Lys	Ser	Gln	Val	Thr	Ile	Ser	Thr	Asp	Thr	Ser	Lys	
				85					90					95		
AAC	CAG	TTC	TCC	CTG	AAG	CTG	AAC	TCT	ATG	ACC	GCC	GCG	GAC	ACG	GCC	336
Asn	Gln	Phe	Ser	Leu	Lys	Leu	Asn	Ser	Met	Thr	Ala	Ala	Asp	Thr	Ala	
			100					105					110			
GTG	TAT	TAC	TGT	GTG	AGA	GAT	CGT	CTT	TTT	TCA	GTT	GTT	GGA	ATG	GTT	384
Val	Tyr	Tyr	Cys	Val	Arg	Asp	Arg	Leu	Phe	Ser	Val	Val	Gly	Met	Val	
	115						120					125				
TAC	AAC	AAC	TGG	TTC	GAT	GTC	TGG	GGC	CCG	GGA	GTC	CTG	GTC	ACC	GTC	432
Tyr	Asn	Asn	Trp	Phe	Asp	Val	Trp	Gly	Pro	Gly	Val	Leu	Val	Thr	Val	
	130					135					140					
TCC	TCA	GCT	AGC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	CCC	CTG	GCA	CCC	TCC	480
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
145					150					155					160	

TCC Ser	AAG Lys	AGC Ser	ACC Thr	TCT Ser 165	GGG Gly	GGC Gly	ACA Thr	GCG Ala	GCC Ala 170	CTG Leu	GGC Gly	TGC Cys	CTG Leu	GTC Val 175	AAG Lys	528
GAC Asp	TAC Tyr	TTC Phe	CCC Pro 180	GAA Glu	CCG Pro	GTG Val	ACG Thr	GTG Val 185	TCG Ser	TGG Trp	AAC Asn	TCA Ser	GGC Gly 190	GCC Ala	CTG Leu	576
ACC Thr	AGC Ser	GGC Gly 195	GTG Val	CAC His	ACC Thr	TTC Phe	CCG Pro 200	GCT Ala	GTC Val	CTA Leu	CAG Gln	TCC Ser 205	TCA Ser	GGA Gly	CTC Leu	624
TAC Tyr 210	TCC Ser	CTC Leu	AGC Ser	AGC Ser	GTG Val	GTG Val 215	ACC Thr	GTG Val	CCC Pro	TCC Ser	AGC Ser 220	AGC Ser	TTG Leu	GGC Gly	ACC Thr	672
CAG Gln 225	ACC Thr	TAC Tyr	ATC Ile	TGC Cys	AAC Asn 230	GTG Val	AAT Asn	CAC His	AAG Lys	CCC Pro 235	AGC Ser	AAC Asn	ACC Thr	AAG Lys	GTG Val 240	720
GAC Asp	AAG Lys	AAA Lys	GCA Ala	GAG Glu 245	CCC Pro	AAA Lys	TCT Ser	TGT Cys	GAC Asp 250	AAA Lys	ACT Thr	CAC His	ACA Thr	TGC Cys 255	CCA Pro	768
CCG Pro	TGC Cys	CCA Pro	GCA Ala 260	CCT Pro	GAA Glu	CTC Leu	CTG Leu	GGG Gly 265	GGA Gly	CCG Pro	TCA Ser	GTC Val	TTC Phe 270	CTC Leu	TTC Phe	816
CCC Pro	CCA Pro	AAA Lys 275	CCC Pro	AAG Lys	GAC Asp	ACC Thr	CTC Leu 280	ATG Met	ATC Ile	TCC Ser	CGG Arg	ACC Thr 285	CCT Pro	GAG Glu	GTC Val	864
ACA Thr 290	TGC Cys	GTG Val	GTG Val	GTG Val	GAC Asp	GTG Val 295	AGC Ser	CAC His	GAA Glu	GAC Asp	CCT Pro 300	GAG Glu	GTC Val	AAG Lys	TTC Phe	912
AAC Asn 305	TGG Trp	TAC Tyr	GTG Val	GAC Asp	GGC Gly 310	GTG Val	GAG Glu	GTG Val	CAT His	AAT Asn 315	GCC Ala	AAG Lys	ACA Thr	AAG Lys	CCG Pro 320	960
CGG Arg	GAG Glu	GAG Glu	CAG Gln 325	TAC Tyr	AAC Asn	AGC Ser	ACG Thr	TAC Tyr	CGT Arg 330	GTG Val	GTC Val	AGC Ser	GTC Val	CTC Leu 335	ACC Thr	1008
GTC Val	CTG Leu	CAC His	CAG Gln 340	GAC Asp	TGG Trp	CTG Leu	AAT Asn	GGC Gly 345	AAG Lys	GAG Glu	TAC Tyr	AAG Lys	TGC Cys 350	AAG Lys	GTC Val	1056
TCC Ser	AAC Asn	AAA Lys 355	GCC Ala	CTC Leu	CCA Pro	GCC Ala	CCC Pro 360	ATC Ile	GAG Glu	AAA Lys	ACC Thr	ATC Ile 365	TCC Ser	AAA Lys	GCC Ala	1104
AAA Lys 370	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAA Glu	CCA Pro 375	CAG Gln	GTG Val	TAC Tyr	ACC Thr	CTG Leu 380	CCC Pro	CCA Pro	TCC Ser	CGG Arg	1152

GAT Asp 385	GAG Glu	CTG Leu	ACC Thr	AAG Lys	AAC Asn 390	CAG Gln	GTC Val	AGC Ser	CTG Leu	ACC Thr 395	TGC Cys	CTG Leu	GTC Val	AAA Lys	GGC Gly 400	1200
TTC Phe	TAT Tyr	CCC Pro	AGC Ser	GAC Asp 405	ATC Ile	GCC Ala	GTG Val	GAG Glu	TGG Trp 410	GAG Glu	AGC Ser	AAT Asn	GGG Gly 415	CAG Gln	CCG Pro	1248
GAG Glu	AAC Asn	AAC Asn	TAC Tyr 420	AAG Lys	ACC Thr	ACG Thr	CCT Pro	CCC Pro 425	GTG Val	CTG Leu	GAC Asp	TCC Ser	GAC Asp 430	GGC Gly	TCC Ser	1296
TTC Phe	TTC Phe	CTC Leu 435	TAC Tyr	AGC Ser	AAG Lys	CTC Leu	ACC Thr 440	GTG Val	GAC Asp	AAG Lys	AGC Ser	AGG Arg 445	TGG Trp	CAG Gln	CAG Gln	1344
GGG Gly 450	AAC Asn	GTC Val	TTC Phe	TCA Ser	TGC Cys	TCC Ser 455	GTG Val	ATG Met	CAT His	GAG Glu	GCT Ala 460	CTG Leu	CAC His	AAC Asn	CAC His	1392
TAC Tyr 465	ACG Thr	CAG Gln	AAG Lys	AGC Ser	CTC Leu 470	TCC Ser	CTG Leu	TCT Ser	CCG Pro	GGT Gly 475	AAA Lys	TGA *				1431

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met 1	Lys	His	Leu	Trp 5	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp 15
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys 30
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile 45
Ser	Gly	Gly	Tyr	Gly	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly 60
Leu 65	Glu	Trp	Ile	Gly	Ser	Phe	Tyr	Ser	Ser	Ser	Gly	Asn	Thr	Tyr	Tyr 80
Asn	Pro	Ser	Leu	Lys	Ser	Gln	Val	Thr	Ile	Ser	Thr	Asp	Thr	Ser	Lys 95
Asn	Gln	Phe	Ser	Leu	Lys	Leu	Asn	Ser	Met	Thr	Ala	Ala	Asp	Thr	Ala 110

Val	Tyr	Tyr	Cys	Val	Arg	Asp	Arg	Leu	Phe	Ser	Val	Val	Gly	Met	Val
		115					120					125			
Tyr	Asn	Asn	Trp	Phe	Asp	Val	Trp	Gly	Pro	Gly	Val	Leu	Val	Thr	Val
	130					135					140				
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser
145					150					155					160
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
				165					170					175	
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
			180					185					190		
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
		195					200					205			
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
	210					215					220				
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
225					230					235					240
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
				245					250					255	
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
			260					265					270		
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
		275					280					285			
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
	290					295					300				
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
305					310					315					320
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
				325					330					335	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
			340					345					350		
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
		355					360					365			
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
	370					375					380				
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
385					390					395					400
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
				405					410					415	

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
420 425 430

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
435 440 445

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
450 455 460

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
465 470 475

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c). —
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.